Kindly replace the paragraph beginning at page 12, line 4 with the following:

A2

--The invention relates to a protein or a peptide consisting or comprising the amino acid sequence shown in figure 2 (SEQ ID NO: 11) or an amino acid sequence having at least 80 %, 90 % and preferably at least 95 % identity or similarity with the amino acid sequence shown in figure 2 (SEQ ID NO: 11). The invention relates also to a protein or a peptide consisting or comprising the amino acid sequence of a functional part of the amino acid sequence shown in figure 2 (SEQ ID NO: 11) or of an amino acid sequence having at least 80 %, 90 % and preferably at least 95 % identity or similarity with a functional part of the amino acid sequence shown in figure 2 (SEQ ID NO: 11). The functional parts, homologous sequences and parts thereof are referred to as "derivatives".--

Kindly replace the paragraph beginning at page 12, line 18 with the following:

A3

--The invention also relates to a functional part of the amino acid sequence shown in Figure 2 (SEQ ID NO: 11) free of the remainder of said amino acid sequence, optionally in association with an amino acid sequence different from said remainder.--

Kindly replace the paragraph beginning at page 13, line 13 with the following:

A4

--A « functional part » is a part which has conserved the function of the protein having the amino acid sequence shown in figure 2 (SEQ ID NO: 11) (RFX-ANK).--

Kindly replace the paragraph beginning at page 13, line 16 with the following:

A5

--The function of the protein having the amino acid sequence shown in figure 2 (SEQ ID NO: 11) (RFX-ANK) can be defined as the capacity to enable the functional transcription of MHC class II genes, via the RFX complex, and consequently the expression of MHC class II gene products.--

Kindly replace the paragraph beginning at page 13, line 22 with the following:

A6

--A function of the protein having the amino acid sequence shown in figure 2 (SEQ ID NO: 11) (RFX-ANK) can be recognised as the capacity to correct the MHC II expression defect of cell lines from patients in complementation group B.--

Kindly replace the paragraph beginning at page 13, line 26 with the following:

A7

--A function of the protein having the amino acid sequence shown in figure 2 (SEQ ID NO: 11) (RFX-ANK) is achieved globally by a series of sequential ~~steps~~ involved.

Kindly replace the paragraph beginning at page 13, line 30 with the following:

A8

--Thus, each of these steps can be considered, in the context of the invention, as being the direct or indirect function of the protein having the amino acid sequence shown in figure 2 (SEQ ID NO: 11) (RFX-ANK).--

(12/97)

Kindly replace the paragraph beginning at page 13, line 34 with the following:

--Consequently, a function of the protein having the amino acid sequence shown in figure 2 (SEQ ID NO: 11) (RFX-ANK) signifies the capacity to allow the expression of MHC class II molecules, to allow the transcription of an MHC class II gene, to allow the expression or the translation of an MHC class II protein or peptide, to allow the formation of the RFX complex, to allow the binding of the RFX complex to its DNA target (especially the X box motif), to allow the interaction between the RFX complex and at least one of the transcription factors X2BP, NF-Y or CIITA, to allow a cooperative interaction that stabilizes the higher order RFX-X2BP-NF-Y complex, to direct contacts between RFX and the co-activator CIITA, to allow binding of RFX5 to the X box, or to correct the MHC II expression defect of cell lines from patients in complementation group B.--

A 9

Kindly replace the paragraph beginning at page 14, line 14 with the following:

--In a preferred embodiment, a function of the protein having the amino acid sequence shown in figure 2 (SEQ ID NO: 11) (RFX-ANK) is to allow the interaction between the RFX complex and CIITA, to allow a cooperative interaction that stabilizes the higher order RFX-X2BP-NF-Y complex, to direct contacts between RFX and the co-activator CIITA or the recruitment of CIITA.--

A 10

Kindly replace the paragraph beginning at page 14, line 21 with the following:

(12/97)

A11

--A « functional part » may not comprise some of the residues of the N-terminal domain of the amino acid sequence shown in figure 2 (SEQ ID NO: 11). In particular, a « functional part » may exclude the 65, 70, 80, 90, 91, 100, 110 first residues of the N-terminal region of the amino acid sequence shown in figure 2 (SEQ ID NO: 11).--

Kindly replace the paragraph beginning at page 14, line 27 with the following:

A12

--The invention relates to a protein or a peptide comprising the amino acid sequence shown in figure 2 (SEQ ID NO: 11) and part thereof, or an amino acid sequence having at least 80 %, 90 % and preferably at least 95 % identity, similarity or homology with the illustrated sequences and part thereof. The homologous sequences and parts thereof are referred to as "derivatives".--

Kindly replace the paragraph beginning at page 15, line 1 with the following:

A13

--The amino acid sequence shown in figure 2 (SEQ ID NO: 11) is the human sequence of RFX-ANK. Derivatives of the figure 2 (SEQ ID NO: 11) sequence may be agonists or antagonists of the RFX-ANK function as defined below.--

Kindly replace the paragraph beginning at page 16, line 24 with the following:

A14

--The nucleic acid molecule of the invention may comprise all or part of the nucleotide sequence illustrated in figure 2 (SEQ ID NO: 10) (GenBank Accession Number: Human RFXANK cDNA AF094760).--

Kindly replace the paragraph beginning at page 17, line 3 with the following:

A15

--In a further embodiment, the invention relates to a nucleic acid molecule comprising the nucleotide sequence illustrated in figure 2 (SEQ ID NO: 10) to a nucleotide sequence exhibiting at least 90 % identity with said nucleotide sequence or to a part of said nucleotide sequence.--

Kindly replace the paragraph beginning at page 19, line 25 with the following:

A16

--The molecule of interest of the present invention is a protein, a peptide or a nucleic acid molecule of the invention encoding said protein or peptide. The molecule is called a transcription factor of the invention. The transcription factors may be RFX-ANK as shown in figure 2 (SEQ ID NO: 10) or derivatives thereof as described earlier.--

Kindly replace the paragraph beginning at page 33, line 1 with the following:

A17

--Said product may particularly be a DNA molecule coding for RFXANK as it is shown in figure 2 (SEQ ID NO: 10), any DNA sequence with at least 80 % identity, preferably 90 % identity with said DNA molecule or any part of said DNA molecule or said DNA sequence.--

Kindly replace the heading at page 45, line 3 with the following:

A18 **--Figure 2 (SEQ ID NOS: 10 and 11): Sequence analyses of RFXANK.--**

(12/97)

Kindly replace the paragraph beginning at page 45, line 14 with the following:

A 19

--**Figure 3 (SEQ ID NOS: 12, 13, 18 and 19): Sequences comparisons**

Amino acid sequence alignment between RFXANK and homologous proteins containing ankyrin repeats. The human RFXANK sequence is shown at the top (Hs RFXANK) (SEQ ID NO: 12). Identical amino acids in mouse RFXANK (Mm RFXANK) (SEQ ID NO: 13) and the other proteins are shown as dashes. Gaps are represented by points. 'Hs homol' (SEQ ID NO: 18) and 'Mm homol' (SEQ ID NO: 19) correspond to the predicted translation products of cDNAs encoding a highly homologous protein present in humans and mice, respectively. The ankyrin repeat-containing region of mouse GABPb (ref. 28) is shown at the bottom. The secondary structure prediction of the ankyrin repeats (ank 1-3) was inferred from the known structure of GABPb (ref. 35). H, helix; T, turn

Kindly replace the heading at page 46, line 10 with the following:

A 20

--**Figure 5 (SEQ ID NOS: 14, 15, 16 AND 17):**--

Kindly replace the paragraph beginning at page 55, line 25 with the following:

A21

--Perfect matches to three independent peptides (Fig. 2a) (SEQ ID NO: 11) were identified in a variety of ESTs as well as in the theoretical protein product deduced from a gene identified by genomic DNA sequencing (GenBank accession number 2627294). The complete sequence of the corresponding mRNA (Fig. 2a) (SEQ ID NO: 10) was

(12/97)

A31 cont'd determined by assembling the ESTs into a single contig and by comparing it to the genomic sequence.--

Kindly replace the paragraph beginning at page 56, line 18 with the following:

A32 --The resulting sequence was confirmed by comparison with the genomic sequence and by RT-PCR amplification and sequencing of RFXANK cDNA clones from control B cell lines (Raji and QBL). The following primers were used to amplify RFXANK cDNAs by PCR: 5'p33 (5'- CCGTACGCGTCTAGACCATGGAGCTTACCCAGCCTGCAGA-3') (SEQ ID NO: 1), which overlaps the translation initiation codon, and 3'p33 (5'-TTCGAATTCTCGAGTGTCTGAGTCCCCGGCA-3') (SEQ ID NO: 2), which is complementary to the 3' untranslated region of RFXANK mRNA. Homology to RFXANK mRNA is underlined. The primers contain restriction sites at their 5' ends to facilitate cloning. RFXANK cDNAs were cloned into the expression plasmid EBO-76PL (ref.[8]) and pBluescript KS (Stratagene). 12 RFXANK cDNA clones were sequenced on both strands. The nucleotide and amino acid sequences of human RFXANK were tested for homology to sequences in EMBL, GenBank, SwissProt, and dbEST. Sequence analysis was performed with PC/gene (Intelligenetics), BLAST programs available through the NCBI server (http://www.ncbi.nlm.nih.gov), and a variety of proteomics tools (http://www.expasy.ch/www/tools.html). For multiple protein sequence alignments, CLUSTALW (http://www2.ebi.ac.uk/clustalw) was used. ESTs were assembled into contigs with the TIGR Assembler (http://www.tigr.org). The search for homology to

human RFXANK identified EST clones corresponding to mouse (AA435121, AA616119, AA259432, AA146531) and rat (AA851701) orthologs, and to a highly homologous gene present in both man (AA496038, AA442702, AA205305, N25678, N70046, AA418029, AA633452, H39858, R86213, AA418089, N64316, R63682, N55216) and mouse (AA245178, Z31339, AA118335). The sequences of mouse Rfxank and of the human and mouse homologues were determined by organizing the corresponding ESTs into contigs. The mouse Rfxank sequence was confirmed by amplifying the cDNA by RT-PCR from C57BL6 mouse spleen RNA using the following primers :

A22

m5'p33 (5'- CCGTACGCGTCTAGACCATGGAGCCCACTCAGGTTGC -3') (SEQ ID NO: 3), which overlaps the translation initiation codon, and m3'p33 (5'- TTCGAATTCTCGAGTGCCTGGGTTCCAGCAGG -3') (SEQ ID NO: 4), which is complementary to the 3' untranslated region of Rfxank mRNA. Homology to mouse Rfxank mRNA is underlined. The primers included 5' extensions with restriction sites that were used to clone the mouse Rfxank cDNA directly into the EBO-76PL expression vector[8]. 14 clones were sequenced on both strands.--

Cont'd

Kindly replace the paragraph beginning at page 57, line 23 with the following:

A23

--Two splice variants were identified at approximately equal frequencies. They differ only by the insertion of a single CAG triplet (Fig. 2a) (SEQ ID NO: 10) and probably result from the alternative usage of two possible splice acceptor sites situated 3 nucleotides apart upstream of exon 4. An additional minor splice variant lacking exon 5

A23 cont'd (see Fig. 2a) (SEQ ID NO: 10) was also identified, both in an EST and in one of the cDNA clones (data not shown).--

Kindly replace the paragraph beginning at page 57, line 32 with the following:

A24 --The cDNA corresponding to the 33 kDa protein contains a 260 amino acid open reading frame. The translation initiation codon is preceded by an in-frame TGA stop codon, indicating that the coding region is complete. The deduced molecular weight (28.1 kDa) and isoelectric point (4.45) correspond well to the biochemical parameters determined for p33 in one- and two-dimensional gel electrophoresis (data not shown). The protein encoded by the open reading frame is novel. In particular, it exhibits no homology to either RFXAP or RFX5, the two other known subunits of the RFX complex, nor to other members of the RFX family of DNA binding proteins[24]. A search for homology to known proteins and motifs did identify the presence of three ankyrin repeats (Fig. 2b) (SEQ ID NO: 11). Together with the fact that it is an essential subunit of the RFX complex, this led us to call the protein RFXANK. Outside of the ankyrin repeat region, the only other recognizable feature is an N-terminal acidic region resembling transcription activation domains.--

Kindly replace the paragraph beginning at page 58, line 16 with the following:

A25 --EST clones corresponding to mouse and rat Rfxank were also identified in the data base. Mouse ESTs were organized into a contig to generate a partial mouse sequence,

A25 Concl.

which was then confirmed and completed by isolating mouse Rfxank cDNA clones by RT-PCR. Homology to human RFXANK is high (85 % overall amino acid identity), particularly within and surrounding the ankyrin repeat region (94% amino acid identity, Fig. 2b) (SEQ ID NO: 11). Two different splice variants were found among mouse Rfxank cDNA clones. The major one, which is shown as the deduced amino acid sequence aligned with the human sequence in Fig. 2b (SEQ ID NO: 10), is characterized by an additional stretch of 10 amino acids that precedes the first ankyrin repeat. A minor splice variant lacking these additional 10 amino acids was also represented among the mouse cDNA clones isolated (not shown). RFXANK may belong to a family of related proteins because we identified a number of additional EST clones corresponding to at least one human and one mouse gene exhibiting a high degree of homology to RFXANK gene (Fig 2b) (SEQ ID NO: 10). These are by far the most closely related sequences currently present in the data base. In addition, the ankyrin repeats of RFXANK show distinct but more limited homology (25-40% identity) to ankyrin repeat regions of a variety of other proteins[20,21], including the b subunit of the transcription factor GABP (ref.[28,29], see Fig. 2b) (SEQ ID NO: 10).--

Kindly replace the paragraph beginning at page 60, line 33 with the following:

A26

--The entire coding region of RFXANK mRNA was amplified by RT-PCR from patient cells using the 5'p33 and 3'p33 primers described above. PCR products were subcloned into pBluescript and sequenced on both strands. For each patient, 3 independent cDNA clones were sequenced. The genomic DNA spanning exons 4 to 7 was amplified by PCR from patient cells using an exon 4 specific primer (5'-CCAGCTCTAGACTCCACCACTCTCACCAAC-3') (SEQ ID NO: 5) having a 5' extension containing an XbaI site (underlined) and an exon 7 specific primer (5'-CCTTCGAATTCTCGCTCTTTTGCCAGGATG-3') (SEQ ID NO: 6) having a 5' extension containing an EcoRI site. PCR products were sublconed into pBluescript KS (Stratagene) and 6 independent subclones were sequenced for each patient. Analysis of the wild type and deleted alleles in the patients and their families was done by PCR using intronic primers flanking exon 6; (5'-GGTTCTCTAGATTGGCAGCACTGGGGATAG-3') (SEQ ID NO: 7) and (5'-GCTACGAATTCCAGCAGACACAGCCAAAAC-3') (SEQ ID NO: 8). These primers carry 5' extensions containing, respectively, XbaI and EcoRI sites (underlined). The sizes of the wild type and deleted PCR products are, respectively, 265 bp, 239 bp (Ab and Na) and 207 bp (BLS1).--

Kindly replace the paragraph beginning at page 61, line 22 with the following:

A27

--Analysis of several independent cDNA clones revealed the presence in all three patients of the same aberrant form of RFXANK mRNA lacking exons 5 and 6 (Fig. 4a).

A27 Cont'd Splicing of exon 4 to exon 7 leads to a frame shift followed by an out of frame stop codon (Fig. 4a) and thus results in the synthesis of a severely truncated RFXANK protein lacking the entire ankyrin repeat region (see Fig. 2b) (SEQ ID NO: 10).--

Kindly replace the paragraph beginning at page 62, line 30 with the following:

A28 --In vitro transcription-translation reactions and electrophoretic mobility shift assays (EMSA) using nuclear extracts and in vitro translated proteins were done as described9,22,50. The production of polyclonal rabbit antisera specific for RFX5 and RFXAP and their use in supershift experiments have also been described10. The monoclonal anti-FLAG antibody (M2, Kodak) was used in supershift experiments at a final concentration of 20 ng/ml. The RFXANK cDNA tagged with a FLAG epitope at its N terminus was constructed as follows: The entire RFXANK open reading frame was amplified from pEBO-RFXANK plasmid by PCR with primers 3'p33 (described above) and FLAG-5'p33 (5'-CCGTACGCGTCTAGAATGGATTACAAAGACGATGACGATAAGATGGAGCTTACCCAGCCTGCAGAAGAC -3') (SEQ ID NO: 9). The FLAG epitope (DYKDDDDK) coding sequence is underlined. The PCR product containing the FLAG sequence fused to the 5' end of RFXANK was cloned in pBluescript KS (Stratagene).--

(12/97)